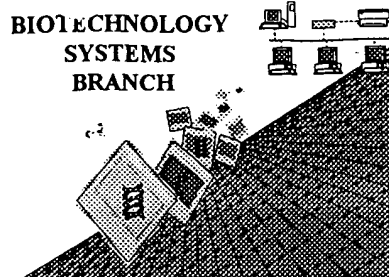


RAW SEQUENCE LISTING **ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/903,188
Source: OIPE
Date Processed by STIC: 7/26/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/903,188

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length
Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
 (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220>
Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/903,188

DATE: 07/26/2001

TIME: 14:58:54

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\07262001\I903188.raw

Does Not Comply
Corrected Diskette Needed

SEQUENCE LISTING

5 (1) GENERAL INFORMATION:

7 (i) APPLICANT: De Robertis, Edward M.
8 Bouwmeester, Tewis10 (ii) TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing
11 Factors

13 (iii) NUMBER OF SEQUENCES: 10

15 (iv) CORRESPONDENCE ADDRESS:

16 (A) ADDRESSEE: Majestic, Parsons, Siebert & Hsue

17 (B) STREET: Four Embarcadero Center, Suite 1100

18 (C) CITY: San Francisco

19 (D) STATE: California

20 (E) COUNTRY: U.S.A.

21 (F) ZIP: 94111-4106

23 (v) COMPUTER READABLE FORM:

24 (A) MEDIUM TYPE: Floppy disk

25 (B) COMPUTER: IBM PC compatible

26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

29 (vi) CURRENT APPLICATION DATA:

30 (A) APPLICATION NUMBER: US/09/903,188

31 (B) FILING DATE: 11-Jul-2001

32 (C) CLASSIFICATION:

34 (vii) PRIOR APPLICATION DATA:

35 (A) APPLICATION NUMBER: US 60/020,150

36 (B) FILING DATE: 20-JUN-1996

38 (viii) ATTORNEY/AGENT INFORMATION:

39 (A) NAME: Siebert, J. Suzanne

40 (B) REGISTRATION NUMBER: 28,758

41 (C) REFERENCE/DOCKET NUMBER: 3100.002US1

43 (ix) TELECOMMUNICATION INFORMATION:

44 (A) TELEPHONE: 415/248-5500

45 (B) TELEFAX: 415/362-5418

ERRORED SEQUENCES

330 (2) INFORMATION FOR SEQ ID NO: 5:

332 (i) SEQUENCE CHARACTERISTICS:

333 (A) LENGTH: 979 amino acids

334 (B) TYPE: amino acid

335 (D) TOPOLOGY: linear

337 (ii) MOLECULE TYPE: peptide

339 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

341 Met Leu Leu Phe Arg Ala Ile Pro Met Leu Leu Leu Gly Leu Met

342 1 5 10 15

344 Val Leu Gln Thr Asp Cys Glu Ile Ala Gln Tyr Tyr Ile Asp Glu Glu

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/903,188

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Input Set : A:\seqlist.txt

Output Set: N:\CRF3\07262001\I903188.raw

```

345          20          25          30
347 Glu Pro Pro Gly Thr Val Ile Ala Val Leu Ser Gln His Ser Ile Phe
348          35          40          45
350 Asn Thr Thr Asp Ile Pro Ala Thr Asn Phe Arg Leu Met Lys Gln Phe
351          50          55          60
353 Asn Asn Ser Leu Ile Gly Val Arg Glu Ser Asp Gly Gln Leu Ser Ile
354 65          70          75          80
356 Met Glu Arg Ile Asp Arg Glu Gln Ile Cys Arg Gln Ser Leu His Cys
357          85          90          95
359 Asn Leu Ala Leu Asp Val Val Ser Phe Ser Lys Gly His Phe Lys Leu
360          100          105          110
362 Leu Asn Val Lys Val Glu Val Arg Asp Ile Asn Asp His Ser Pro His
363          115          120          125
365 Phe Pro Ser Glu Ile Met His Val Glu Val Ser Glu Ser Ser Ser Val
366          130          135          140
368 Gly Thr Arg Ile Pro Leu Glu Ile Ala Ile Asp Glu Asp Val Gly Ser
369 145          150          155          160
371 Asn Ser Ile Gln Asn Phe Gln Ile Ser Asn Asn Ser His Phe Ser Ile
372          165          170          175
374 Asp Val Leu Thr Arg Ala Asp Gly Val Lys Tyr Ala Asp Leu Val Leu
375          180          185          190
377 Met Arg Glu Leu Asp Arg Glu Ile Gln Pro Thr Tyr Ile Met Glu Leu
378          195          200          205
380 Leu Ala Met Asp Gly Gly Val Pro Ser Leu Ser Gly Thr Ala Val Val
381          210          215          220
383 Asn Ile Arg Val Leu Asp Phe Asn Asp Asn Ser Pro Val Phe Glu Arg
384 225          230          235          240
386 Ser Thr Ile Ala Val Asp Leu Val Glu Asp Ala Pro Leu Gly Tyr Leu
387          245          250          255
389 Leu Leu Glu Leu His Ala Thr Asp Asp Asp Glu Gly Val Asn Gly Glu
390          260          265          270
392 Ile Val Tyr Gly Phe Ser Thr Leu Ala Ser Gln Glu Val Arg Gln Leu
393          275          280          285
395 Phe Lys Ile Asn Ser Arg Thr Gly Ser Val Thr Leu Glu Gly Gln Val
396          290          295          300
398 Asp Phe Glu Thr Lys Gln Thr Tyr Glu Phe Glu Val Gln Ala Gln Asp
399 305          310          315          320
401 Leu Gly Pro Asn Pro Leu Thr Ala Thr Cys Lys Val Thr Val His Ile
402          325          330          335
404 Leu Asp Val Asn Asp Asn Thr Pro Ala Ile Thr Ile Thr Pro Leu Thr
405          340          345          350
407 Thr Val Asn Ala Gly Val Ala Tyr Ile Pro Glu Thr Ala Thr Lys Glu
408          355          360          365
410 Asn Phe Ile Ala Leu Ile Ser Thr Thr Asp Arg Ala Ser Gly Ser Asn
411          370          375          380
413 Gly Gln Val Arg Cys Thr Leu Tyr Gly His Glu His Phe Lys Leu Gln
414 385          390          395          400
416 Gln Ala Tyr Glu Asp Ser Tyr Met Ile Val Thr Thr Ser Thr Leu Asp
417          405          410          415

```


RAW SEQUENCE LISTING

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Input Set : A:\seqlist.txt

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```

419 Arg Glu Asn Ile Ala Ala Tyr Ser Leu Thr Val Val Ala Glu Asp Leu
420                420                425                430
422 Gly Phe Pro Ser Leu Lys Thr Lys Lys Tyr Tyr Thr Val Lys Val Ser
423                435                440                445
425 Asp Glu Asn Asp Asn Ala Pro Val Phe Ser Lys Pro Gln Tyr Glu Ala
426                450                455                460
428 Ser Ile Leu Glu Asn Asn Ala Pro Gly Ser Tyr Ile Thr Thr Val Ile
429 465                470                475                480
431 Ala Arg Asp Ser Asp Ser Asp Gln Asn Gly Lys Val Asn Tyr Arg Leu
432                485                490                495
434 Val Asp Ala Lys Val Met Gly Gln Ser Leu Thr Thr Phe Val Ser Leu
435                500                505                510
437 Asp Ala Asp Ser Gly Val Leu Arg Ala Val Arg Ser Leu Asp Tyr Glu
438                515                520                525
440 Lys Leu Lys Gln Leu Asp Phe Glu Ile Glu Ala Ala Asp Asn Gly Ile
441                530                535                540
443 Pro Gln Leu Ser Thr Arg Val Gln Leu Asn Leu Arg Ile Val Asp Gln
444 545                550                555                560
446 Asn Asp Asn Cys Pro Val Ile Thr Asn Pro Leu Leu Asn Asn Gly Ser
447                565                570                575
449 Gly Glu Val Leu Leu Pro Ile Ser Ala Pro Gln Asn Tyr Leu Val Phe
450                580                585                590
452 Gln Leu Lys Ala Glu Asp Ser Asp Glu Gly His Asn Ser Gln Leu Phe
453                595                600                605
455 Tyr Thr Ile Leu Arg Asp Pro Ser Arg Leu Phe Ala Ile Asn Lys Glu
456                610                615                620
458 Ser Gly Glu Val Phe Leu Lys Lys Gln Leu Asn Ser Asp His Ser Glu
459 625                630                635                640
461 Asp Leu Ser Ile Val Val Ala Val Tyr Asp Leu Gly Arg Pro Ser Leu
462                645                650                655
464 Val Ala Asn Arg Met His Ala Glu Tyr Glu Arg Asp Leu Val Asn Arg
E--> 465 930 660 935 665 940 670
467 Ser Ala Thr Leu Ser Pro Gln Arg Ser Ser Ser Arg Tyr Gln Glu Phe
E--> 468 945 675 950 680 955 685 960
470 Asn Tyr Ser Pro Gln Ile Ser Arg Gln Leu His Pro Ser Glu Ile Ala
E--> 471 690 965 695 970 700 975
E--> 473 Thr Thr Phe 705
780 (2) INFORMATION FOR SEQ ID NO: 9:
782 (i) SEQUENCE CHARACTERISTICS:
783 (A) LENGTH: 325 amino acids
784 (B) TYPE: amino acid
785 (D) TOPOLOGY: linear
787 (ii) MOLECULE TYPE: peptide
789 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
791 Met Val Cys Gly Ser Pro Gly Gly Met Leu Leu Leu Arg Ala Gly Leu
E--> 792 1 5 10 15
794 Leu Ala Leu Ala Ala Leu Cys Leu Leu Arg Val Pro Gly Ala Arg Ala
795 20 25 30
797 Ala Ala Cys Glu Pro Val Arg Ile Pro Leu Cys Lys Ser Leu Pro Trp

```

*misaligned
amino acid has.
(see item 3
on Ena
summary
sheet)*

RAW SEQUENCE LISTING

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```

798          35          40          45
800 Asn Met Thr Lys Met Pro Asn His Leu His His Ser Thr Gln Ala Asn
801          50          55          60
803 Ala Ile Leu Ala Ile Glu Gln Phe Glu Gly Leu Leu Gly Thr His Cys
804 65          70          75          80
806 Ser Pro Asp Leu Leu Phe Phe Leu Cys Ala Met Tyr Ala Pro Ile Cys
807          85          90          95
809 Thr Ile Asp Phe Gln His Glu Pro Ile Lys Pro Cys Lys Ser Val Cys
810          100          105          110
812 Glu Arg Ala Arg Gln Gly Cys Glu Pro Ile Leu Ile Lys Tyr Arg His
813          115          120          125
815 Ser Trp Pro Glu Asn Leu Ala Cys Glu Glu Leu Pro Val Tyr Asp Arg
816          130          135          140
818 Gly Val Cys Ile Ser Pro Glu Ala Ile Val Thr Ala Asp Gly Ala Asp
819 145          150          155          160
821 Phe Pro Met Asp Ser Ser Asn Gly Asn Cys Arg Gly Ala Ser Ser Glu
822          165          170          175
824 Arg Cys Lys Cys Lys Pro Ile Arg Ala Thr Gln Lys Thr Tyr Phe Arg
825          180          185          190
827 Asn Asn Tyr Asn Tyr Val Ile Arg Ala Lys Val Lys Glu Ile Lys Thr
828          195          200          205
830 Lys Cys His Asp Val Thr Ala Val Val Glu Val Lys Glu Ile Leu Lys
831          210          215          220
833 Ser Ser Leu Val Asn Ile Pro Arg Asp Thr Val Asn Leu Tyr Thr Ser
834 225          230          235          240
836 Ser Gly Cys Leu Cys Pro Pro Leu Asn Val Asn Glu Glu Tyr Ile Ile
837          245          250          255
839 Met Gly Tyr Glu Asp Glu Glu Arg Ser Arg Leu Leu Leu Val Glu Gly
840          260          265          270
842 Ser Ile Ala Glu Lys Trp Lys Asp Arg Leu Gly Lys Lys Val Lys Arg
843          275          280          285
845 Trp Asp Met Lys Leu Arg His Leu Gly Leu Ser Lys Ser Asp Ser Ser
846          290          295          300
848 Asn Ser Asp Ser Thr Gln Ser Gln Lys Ser Gly Arg Asn Ser Asn Pro
849 305          310          315          320
851 Arg Gln Ala Arg Asn
852          325

```


VERIFICATION SUMMARY

PATENT APPLICATION: US/09/903,188

DATE: 07/26/2001

TIME: 14:58:55

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\07262001\I903188.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:465 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5
M:332 Repeated in SeqNo=5
L:473 M:203 E: No. of Seq. differs, LENGTH:Input:979 Found:707 SEQ:5
L:792 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:9